

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/525,324A
Source: Pt
Date Processed by STIC: 1/27/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/525,324A

CRF Edit Date: 1/31/06
Edited by: [signature]

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓
___ Other:
Sequence 14 - used numeral "1" and numeral "0" in amino acid numbering (instead of letter "l" and letter "O")

Sequence 2 - replaced numeral "1" in "Artificial" with letter "l"

Revised 09/09/2003



PCT

RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/525,324A

TIME: 14:48:13

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01312006\J525324A.raw

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3 <110> APPLICANT: SAKI, Mayumi
4     NONAKA, Hiromi
5     MIYAJI, Hiromasa
6     ICHIKAWA, Shunji
7     TAKASHIMA, Chiemi
8     MATSUMURA, Tsutomu
9     ARAI, Hitoshi
10    SASAKI, Katsutoshi
11    KOBATAKE, Choei
12    TSUKUMO, Yukihito
13    IIDA, Kyoichiro
14    KUBOYAMA, Takeshi
15    MANABE, Haruhiko
17 <120> TITLE OF INVENTION: Agent for prevention and/or treatment of itching
19 <130> FILE REFERENCE: 506.44793X00
21 <140> CURRENT APPLICATION NUMBER: US/10/525,324A
22 <141> CURRENT FILING DATE: 2005-02-22
24 <150> PRIOR APPLICATION NUMBER: JP 2002/241522
25 <151> PRIOR FILING DATE: 2002-08-22
27 <160> NUMBER OF SEQ ID NOS: 20
29 <170> SOFTWARE: PatentIn Ver 2.1
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34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Synthetic DNA
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43 <210> SEQ ID NO: 2
44 <211> LENGTH: 54
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Synthetic DNA
51 <400> SEQUENCE: 2
52 tgcattgaaa aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta tttg 54
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 39
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic DNA

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Input Set : A:\PTO.AMC.txt

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62 <400> SEQUENCE: 3
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66 <211> LENGTH: 39
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: Synthetic DNA
73 <400> SEQUENCE: 4
74 gtacccccgg gctcgagttt ggacaaacca caactagaa      39
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 40
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Synthetic DNA
84 <400> SEQUENCE: 5
85 tcgacggtat cgattcgact gacgtcatatc ttgacgtcac      40
89 <210> SEQ ID NO: 6
90 <211> LENGTH: 40
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Synthetic DNA
97 <400> SEQUENCE: 6
98 tcgagtgcgc tcaagtatga cgtcagtcga atcgataccg      40
102 <210> SEQ ID NO: 7
103 <211> LENGTH: 29
104 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Synthetic DNA
111 <400> SEQUENCE: 7
112 gccccagaag cttaagtgcc caccatggg      29
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 33
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Synthetic DNA
124 <400> SEQUENCE: 8
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131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Synthetic DNA
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Input Set : A:\PTO.AMC.txt

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138 cggagactct agagggtata taatg          25
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144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
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154 <211> LENGTH: 362
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 11
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160   1          5          10          15
162 His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu
163          20          25          30
165 Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln
166          35          40          45
168 Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu
169          50          55          60
171 Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His
172 65          70          75          80
174 Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile
175          85          90          95
177 Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser
178          100         105         110
180 Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu
181          115         120         125
183 Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr
184          130         135         140
186 Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg
187 145         150         155         160
189 Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly
190          165         170         175
192 Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe
193          180         185         190
195 Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val
196          195         200         205
198 Arg Gly Ser Val Ser Thr Gln Arg Gln Glu Lys Ala Lys Ile Lys Arg
199          210         215         220
201 Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr
202 225         230         235         240
204 His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp
205          245         250         255
207 Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu
208          260         265         270
210 Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu

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211          275          280          285
213 Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu
214          290          295          300
216 Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser
217 305          310          315          320
219 Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys
220          325          330          335
222 Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln
223          340          345          350
225 Val Gln Leu Lys Met Leu Pro Pro Ala Gln
226          355          360
228 <210> SEQ ID NO: 12
229 <211> LENGTH: 2932
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 12
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235 ggagtccttc cctgcccc attgaaattt cccttcgcgc cccaaactta cctctgatct 120
236 agaccttact cacctccttc ctgtttccta agactccttc ctgccgtcca cagaccgagc 180
237 cttttatctt tgtccacct gtgccagaca cctccttttc cagaaccttc tccttactgg 240
238 tgaccttact tatctctgtt gctttctggg gtcctaggaa atgccagcac tcccaccac 300
239 attgcctgaa ctttccaaca ctccctagct gcgctgtgtc ctatctcaac acttccctcat 360
240 gtatttcttg tgtcttctag aacattcccc cgccattatt acttcaatat ggctacacat 420
241 acttccctaat tgccctgcaa accatctcct tctcaccatt gcccgagcat gctttcgtct 480
242 cctccataaa cactcccggg gaccaatttt tgtgtcaccc ccatactccc tcgttgacac 540
243 actgactcca tacataacct ccttgaaaaa cctctttatt aatctcacca tcctccagac 600
244 ttcctcctcg tcataattcc atccctcctc caacttttcc ctctcaagct ctgcccttcc 660
245 cagcccagcc cagcctaccc aacctcatct ctccctgta gaccacatcc caccatgttc 720
246 ccctgagcct ccaaggaagg ggctcagggg gcccctggc ctcccgtcc ctgtggcccc 780
247 acagcccccg tgggccaggg gaagcgcccc agaagccgaa gtgcccacc atg ggc aac 838
248                                     Met Gly Asn
249                                     1
251 cac acg tgg gag ggc tgc cac gtg gac tcg cgc gtg gac cac ctc ttt 886
252 His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe
253          5          10          15
255 ccg cca tcc ctc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac 934
256 Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn
257 20          25          30          35
259 tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag 982
260 Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu
261          40          45          50
263 ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030
264 Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile
265          55          60          65
267 tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg 1078
268 Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp
269          70          75          80
271 atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc 1126
272 Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr

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file:///C:/CRF4/OUTHOLD/VsrJ525324A.htm

VERIFICATION SUMMARY

DATE: 01/31/2006

PATENT APPLICATION: US/10/525,324A

TIME: 14:48:14

Input Set : A:\PTO.AMC.txt

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**Raw Sequence Listing before editing
(for reference only)**



PCT

RAW SEQUENCE LISTING

DATE: 01/27/2006

PATENT APPLICATION: US/10/525,324A

TIME: 09:50:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

3 <110> APPLICANT: SAKI, Mayumi
 4 NONAKA, Hiromi
 5 MIYAJI, Hiromasa
 6 ICHIKAWA, Shunji
 7 TAKASHIMA, Chiemi
 8 MATSUMURA, Tsutomu
 9 ARAI, Hitoshi
 10 SASAKI, Katsutoshi
 11 KOBATAKE, Choei
 12 TSUKUMO, Yukihiro
 13 IIDA, Kyoichiro
 14 KUBOYAMA, Takeshi
 15 MANABE, Haruhiko
 17 <120> TITLE OF INVENTION: Agent for prevention and/or treatment of itching
 19 <130> FILE REFERENCE: 506.44793X00
 21 <140> CURRENT APPLICATION NUMBER: US/10/525,324A
 22 <141> CURRENT FILING DATE: 2005-02-22
 24 <150> PRIOR APPLICATION NUMBER: JP 2002/241522
 25 <151> PRIOR FILING DATE: 2002-08-22
 27 <160> NUMBER OF SEQ ID NOS: 20
 29 <170> SOFTWARE: PatentIn Ver 2.1

ERRORED SEQUENCES

438 <210> SEQ ID NO: 14
 439 <211> LENGTH: 1098
 440 <212> TYPE: DNA
 441 <213> ORGANISM: Mus musculus
 443 <400> SEQUENCE: 14
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 445 Met Asp Asn Ser Thr Gly Thr Gly Glu Gly Cys His Val Asp Ser Arg
 446 1 5 10 15
 448 gtg gac cac ctc ttc cca cca tct ctc tac atc ttc gtc atc ggg gtg 96
 449 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val
 450 20 25 30
 452 ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgg cag gtg 144
 453 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val
 454 35 40 45
 456 cgc caa cac aat gag ctg ggc gtc tac ctg atg aac ttg agc att gca 192
 457 Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala
 458 50 55 60
 460 gac ctg ctg tac atc tgc act ttg ccg ctg tgg gtc gac tac ttc ctc 240

Does Not Comply
 Corrected Diskette Needed

P.2

RAW SEQUENCE LISTING

DATE: 01/27/2006

PATENT APPLICATION: US/10/525,324A

TIME: 09:50:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

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461 Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu
462 65 70 75 80
464 cac cat gac aac tgg atc cac ggc cct ggc tcc tgc aag ctc ttt ggc 288
465 His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly
466 85 90 95
468 ttc atc ttc tac agc aac atc tat atc agc atc gcc ttc ctg tgc tgc 336
469 Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys
470 100 105 110
472 atc tcc gtg gac cgc tac ctg gct gtg gct cat cct ctg cgc ttt gca 384
473 Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala
474 115 120 125
476 cgc ctg cgc cgg gtc aag aca gca gtg gct gtg agc tct gtg gtc tgg 432
477 Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp
478 130 135 140
480 gcc acg gag ctg ggc gcc aat tca gca ccg ctc ttc cat gat gag ctg 480
481 Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu
E--> 482 145 150 155 use number 1 ← 0600 ← use number "φ"
E--> 484 ttt cgt gat cgc tac aac cac acc ttc tgc ttt gag aag ttc ccc atg 528
485 Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met
W--> 486 165 170 175
E--> 488 gag cgt tgg gtg gcc tgg atg aat ctg tac cgc gtc ttt gtg ggc ttc 576
489 Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe
490 180 185 190
E--> 492 ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgt ggc atc ctg agg 624
493 Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg
494 195 200 205
E--> 496 gca gtg cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc 672
497 Ala Val Gln Ser Ser Val Ser Thr Glu Arg Glu Glu Lys Val Lys Ile
498 210 215 220
E--> 500 aaa cgt ctg gcc ctg agc ctc atc gcc att gtg ctg gtg tgc ttt gcg 720
501 Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala
502 225 230 235 240
E--> 504 cct tac cat gct ctc ctg ctg tct cgc agc gcc gtc tac ctg ggc cgg 768
505 Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg
506 245 250 255
E--> 508 ccc tgg gac tgt ggc ttc gag gag cga gtc ttt tct gcc tac cac agc 816
509 Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser
510 260 265 270
E--> 512 tcc ctg gcc ttc acc agc ctc aat tgt gtg gct gac ccc atc ctc tac 864
513 Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr
514 275 280 285
E--> 516 tgc ctg gtc aac gag ggt gcc cgc agt gat gtg gcc aag gcc ctg cac 912
517 Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His
518 290 295 300
E--> 520 aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat 960
521 Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn
522 305 310 315 320
E--> 524 gct tcc ctc acc ctg gag aca ccc ttg acc tcc aag agg agc acc acc 1008
525 Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr

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DATE: 01/27/2006

TIME: 09:50:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

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E-->	528	ggc	aag	tcg	tcc	ggg	gct	gtc	tgg	gca	gtg	cct	ccg	act	gcc	cag	ggg	1056	
	529	Gly	Lys	Ser	Ser	Gly	Ala	Val	Trp	Ala	Val	Pro	Pro	Thr	Ala	Gln	Gly		
	530					340				345					350				
E-->	532	gac	cag	gtg	cca	ctg	aag	gtg	ctg	ctg	ccc	ccg	gca	cag	tga		1098		
	533	Asp	Gln	Val	Pro	Leu	Lys	Val	Leu	Leu	Pro	Pro	Ala	Gln					
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	639	<212> TYPE: DNA																	
E-->	640	<213> Rattus norvegicus																	
E-->	642	<400> SEQUENCE: 18																	
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	644	Met	Asp	Asn	Ser	Thr	Gly	Thr	Trp	Glu	Gly	Cys	His	Val	Asp	Ser	Arg		
	645	1				5				10					15				
	647	gtg	gac	cac	ctc	ttc	cca	cca	tcc	ctc	tac	atc	ttc	gtc	atc	ggg	gtg	96	
	648	Val	Asp	His	Leu	Phe	Pro	Pro	Ser	Leu	Tyr	Ile	Phe	Val	Ile	Gly	Val		
	649				20				25					30					
	651	ggg	ctg	ccc	acc	aac	tgc	ctg	gcc	ctg	tgg	gca	gcc	tac	cgc	cag	gtg	144	
	652	Gly	Leu	Pro	Thr	Asn	Cys	Leu	Ala	Leu	Trp	Ala	Ala	Tyr	Arg	Gln	Val		
	653			35				40					45						
	655	cgc	cag	cgc	aat	gag	ctg	ggc	gtc	tac	ctg	atg	aac	ttg	agc	atc	gca	192	
	656	Arg	Gln	Arg	Asn	Glu	Leu	Gly	Val	Tyr	Leu	Met	Asn	Leu	Ser	Ile	Ala		
	657		50				55			60									
	659	gac	ctg	ctg	tac	atc	tgt	acg	ctg	ccg	ctg	tgg	gtc	gac	tac	ttc	ctc	240	
	660	Asp	Leu	Leu	Tyr	Ile	Cys	Thr	Leu	Pro	Leu	Trp	Val	Asp	Tyr	Phe	Leu		
	661	65				70				75				80					
	663	cac	cat	gac	aac	tgg	atc	cac	ggc	ccc	ggc	tcc	tgc	aag	ctc	ttt	ggc	288	
	664	His	His	Asp	Asn	Trp	Ile	His	Gly	Pro	Gly	Ser	Cys	Lys	Leu	Phe	Gly		
	665				85					90				95					
	667	ttc	atc	ttc	tac	agc	aac	atc	tac	atc	agc	atc	gcc	ttc	ctg	tgc	tgc	336	
	668	Phe																	

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691 ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgc ggc atc ctg cgg 624
692 Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg
693      195      200      205
695 gcc gta cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc 672
696 Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile
697      210      215      220
699 aaa cgc ctg gcc ctg agc ctc atc gcc atc gtg ctg gtg tgc ttt gca 720
700 Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala
701 225      230      235      240
703 ccc tac cat gct ctc ttg ctg tct cgc agc gct gtc tat ctg ggc cgg 768
704 Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg
705      245      250      255
707 ccc tgg gac tgt ggc ttc gag gag cga gtc ttc tct gcc tac cac agc 816
708 Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser
709      260      265      270
711 tcc cta gcc ttc acc agc ctc aat tgc gtg gct gac ccc atc ctc tac 864
712 Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr
713      275      280      285
715 tgc ctg gtc aac gag ggt gcc cgt agt gac gtg gcc aaa gcc ctg cac 912
716 Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His
717      290      295      300
719 aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat 960
720 Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn
721 305      310      315      320
723 gct tcc ctc acc ctg gag aca cca ttg acc tcc aag agg agc acc acc 1008
724 Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr
725      325      330      335
727 ggc aaa acg tct ggg gct gtc tgg gca gtg cct ccc act gcc cag ggg 1056
728 Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly
729      340      345      350
731 gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga 1098
732 Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln
733      355      360      365

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VERIFICATION SUMMARY

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TIME: 09:50:50

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

L:46 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:482 SEQ:14
L:482 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:484 M:254 E: No. of Bases conflict, LENGTH:Input:528 Counted:530 SEQ:14
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:488 M:254 E: No. of Bases conflict, LENGTH:Input:576 Counted:578 SEQ:14
L:492 M:254 E: No. of Bases conflict, LENGTH:Input:624 Counted:626 SEQ:14
L:496 M:254 E: No. of Bases conflict, LENGTH:Input:672 Counted:674 SEQ:14
L:500 M:254 E: No. of Bases conflict, LENGTH:Input:720 Counted:722 SEQ:14
L:504 M:254 E: No. of Bases conflict, LENGTH:Input:768 Counted:770 SEQ:14
L:508 M:254 E: No. of Bases conflict, LENGTH:Input:816 Counted:818 SEQ:14
L:512 M:254 E: No. of Bases conflict, LENGTH:Input:864 Counted:866 SEQ:14
L:516 M:254 E: No. of Bases conflict, LENGTH:Input:912 Counted:914 SEQ:14
L:520 M:254 E: No. of Bases conflict, LENGTH:Input:960 Counted:962 SEQ:14
L:524 M:254 E: No. of Bases conflict, LENGTH:Input:1008 Counted:1010 SEQ:14
L:528 M:254 E: No. of Bases conflict, LENGTH:Input:1056 Counted:1058 SEQ:14
L:532 M:254 E: No. of Bases conflict, LENGTH:Input:1098 Counted:1100 SEQ:14
L:534 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1098 Found:1100 SEQ:14
L:640 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:642 M:282 E: Numeric Field Identifier Missing, <213> is required.